

SEQUENCE LISTING



<110> Finlay, Brett B
Kenny, Brendan
DeVinney, Rebekah
Stein, Markus

<120> HOST RECEPTOR FOR PATHOGENIC BACTERIA

<130> 07422/013001

<140> 09/189,415

<141> 1998-11-10

<150> 60/065,130

<151> 1997-11-12

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<170> PatentIn Ver. 2.0

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Leu Phe Ser Pro Leu Arg Asn Ser Met Ala Asp Ser Val Asp Ser Arg
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Asp Ile Pro Gly Leu Pro Thr Asn Pro Ser Arg Leu Ala Ala Ala Thr
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Ser Glu Thr Cys Leu Leu Gly Gly Phe Glu Val Leu His Asp Lys Gly
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Pro Leu Asp Ile Leu Asn Thr Gln Ile Gly Pro Ser Ala Phe Arg Val
100 105 110

Glu Val Gln Ala Asp Gly Thr His Ala Ala Ile Gly Glu Lys Asn Gly
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Ser Ile Asp Thr Glu Gly Lys Asn Arg Phe Val Phe Thr Gly Gly Arg
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Arg	Gln	Pro	Lys	Asp	Val	Asp	Thr	Arg	Ser	Val	Gly	Val	Gly	Ser	Ala	195	200	205
Ser	Gly	Ile	Asp	Asp	Gly	Val	Val	Ser	Glu	Thr	His	Thr	Ser	Thr	Thr	210	215	220
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Glu	Ala	Phe	Lys	Asn	Pro	Glu	Asn	Gln	Lys	Val	Asn	Ile	Asp	Ala	Asn	290	295	300
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Ser	Ser	Ala	Leu	Ile	Val	Ala	Gly	Gly	Ile	Gly	Ala	Gly	Val	Thr	Thr	370	375	380
Ala	Leu	His	Arg	Arg	Asn	Gln	Pro	Ala	Glu	Gln	Thr	Thr	Thr	Thr	Thr	385	390	395
Thr	His	Thr	Val	Val	Gln	Gln	Gln	Thr	Gly	Gly	Ile	Pro	Gln	His	Lys	405	410	415

Val Ala Leu Met Pro Gln Glu Arg Arg Arg Phe Ser Asp Arg Arg Asp
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Ser Gln Gly Ser Val Ala Ser Thr His Trp Ser Asp Ser Ser Ser Glu
 435 440 445

Val Val Asn Pro Tyr Ala Glu Val Gly Gly Ala Arg Asn Ser Leu Ser
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Ala His Gln Pro Glu Glu His Ile Tyr Asp Glu Val Ala Ala Asp Pro
 465 470 475 480

Gly Tyr Ser Val Ile Gln Asn Phe Ser Gly Ser Gly Pro Val Thr Gly
 485 490 495

Arg Leu Ile Gly Thr Pro Gly Gln Gly Ile Gln Ser Thr Tyr Ala Leu
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Leu Ala Asn Ser Gly Gly Leu Arg Leu Gly Met Gly Gly Leu Thr Ser
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Pro Val Arg Phe Val
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35 40 45

Thr Pro Val Arg Asn Ser Met Ala Asp Ser Gly Asp Asn Arg Ala Ser
50 55 60

Asp Val Pro Gly Leu Pro Val Asn Pro Met Arg Leu Ala Ala Ser Glu
65 70 75 80

Ile Thr Leu Asn Asp Gly Phe Glu Val Leu His Asp His Gly Pro Leu
85 90 95

Asp Thr Leu Asn Arg Gln Ile Gly Ser Ser Val Phe Arg Val Glu Thr
100 105 110

Gln Glu Asp Gly Lys His Ile Ala Val Gly Gln Arg Asn Gly Val Glu
115 120 125

Thr Ser Val Val Leu Ser Asp Gln Glu Tyr Ala Arg Leu Gln Ser Ile
130 135 140

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Gln	Arg	Ile	Leu	Glu	Leu	Leu	Glu	Pro	Lys	Gly	Thr	Gly	Glu	Ser	Lys			180	185	190	
Gly	Ala	Gly	Glu	Ser	Lys	Gly	Val	Gly	Glu	Leu	Arg	Glu	Ser	Asn	Ser			195	200	205	
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Ser	Ala	Thr	Glu	Thr	Ala	Thr	Arg	Asp	Gln	Leu	Thr	Lys	Glu	Ala	Phe			275	280	285	
Gln	Asn	Pro	Asp	Asn	Gln	Lys	Val	Asn	Ile	Asp	Glu	Leu	Gly	Asn	Ala			290	295	300	
Ile	Pro	Ser	Gly	Val	Leu	Lys	Asp	Asp	Val	Val	Ala	Asn	Ile	Glu	Glu			305	310	315	320
Gln	Ala	Lys	Ala	Ala	Gly	Glu	Glu	Ala	Lys	Gln	Gln	Ala	Ile	Glu	Asn			325	330	335	
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Glu	Glu	Leu	Lys	Val	Ser	Ser	Gly	Ala	Gly	Tyr	Gly	Leu	Ser	Gly	Ala			355	360	365	
Leu	Ile	Leu	Gly	Gly	Gly	Ile	Gly	Val	Ala	Val	Thr	Ala	Ala	Leu	His			370	375	380	
Arg	Lys	Asn	Gln	Pro	Val	Glu	Gln	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr			385	390	395	400

Thr Thr Thr Ser Ala Arg Thr Val Glu Asn Lys Pro Ala Asn Asn Thr
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Pro Ala Gln Gly Asn Val Asp Thr Pro Gly Ser Glu Asp Thr Met Glu
 420 425 430

Ser Arg Arg Ser Ser Met Ala Ser Thr Ser Ser Thr Phe Phe Asp Thr
 435 440 445

Ser Ser Ile Gly Gly Pro Cys Arg Ile Arg Met Leu Met Leu Lys His
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Arg Cys Met Ile Arg Arg Cys Arg Leu Leu Ile Leu Ile Arg Leu Phe
 465 470 475 480

Arg Ile Trp Gly Ile Gln Ile Ser Val Val Tyr Ser Thr Ile Gln His
 485 490 495

Pro Pro Arg Asp Thr Thr Asp Asn Gly Ala Arg Leu Leu Gly Asn Pro
 500 505 510

Ser Ala Gly Ile Gln Ser Thr Tyr Ala Arg Leu Ala Leu Ser Gly Gly
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Ser Ala Ile Gly Ser Ser Leu Phe Arg Val Glu Thr Arg Asp Asp Gly
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Ser His Val Ala Ile Gly Gln Lys Asn Gly Leu Glu Thr Thr Val Val
65 70 75 80

Leu Ser Glu Gln Glu Phe Ser Ser Leu Gln Ser Leu Asp Pro Glu Gly
85 90 95

Lys Asn Lys Phe Val Phe Thr Gly Gly Arg Gly Gly Pro Gly His Ala
100 105 110

Met Val Thr Val Ala Ser Asp Ile Ala Glu Ala Arg Gln Arg Ile Ile
115 120 125

Asp Lys Leu Glu Pro Lys Asp Thr Lys Glu Thr Lys Glu Pro Gly Asp
130 135 140

Pro	Asn	Ser	Gly	Glu	Gly	Lys	Ile	Ile	Glu	Ile	His	Thr	Ser	Thr	Ser		
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Ile	Ala	Ala	Gly	Leu	Ile	Gly	Met	Ala	Ala	Thr	Gly	Ile	Ala	Gln	Ala		
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Val	Ala	Leu	Thr	Pro	Glu	Pro	Asp	Asp	Pro	Ile	Thr	Thr	Asp	Pro	Asp		
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Ala	Ala	Ala	Asn	Thr	Ala	Glu	Ala	Ala	Ala	Lys	Asp	Gln	Leu	Thr	Lys		
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Glu	Ala	Phe	Gln	Asn	Pro	Asp	Asn	Gln	Lys	Val	Asn	Ile	Asp	Glu	Asn		
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Ala	Leu	His	Arg	Lys	Asn	Gln	Pro	Ala	Glu	Gln	Thr	Ile	Thr	Thr	Arg		
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Thr	Val	Val	Asp	Asn	Gln	Pro	Thr	Asn	Asn	Ala	Ser	Ala	Gln	Gly	Asn		
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Thr	Asp	Thr	Ser	Gly	Pro	Glu	Glu	Ser	Pro	Ala	Ser	Arg	Arg	Asn	Ser		
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Asn	Ala	Ser	Leu	Ala	Ser	Asn	Gly	Ser	Asp	Thr	Ser	Ser	Thr	Gly	Thr		
	370					375					380						
Val	Glu	Asn	Pro	Tyr	Ala	Asp	Val	Gly	Met	Pro	Arg	Asn	Asp	Ser	Leu		
385					390					395					400		

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Asn Tyr Ser Val Ile Gln His Phe Ser Gly Asn Ser Pro Val Thr Gly
420 425 430

Arg Leu Val Gly Thr Pro Gly Gln Gly Ile Gln Ser Thr Tyr Ala Leu
435 440 445

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450 455 460

Gly Gly Glu Ser Ala Val Ser Thr Ala Asn Ala Ala Thr Pro Gly Pro
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Ala Arg Phe Val

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<213> Artificial Sequence

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SEQUENCE

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<210> 9
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